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Spent Medium Recycling and Characterization for the Cultivation of *Chlorella sorokiniana* Microalgae

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Abstract

Microalgae has gained substantial attention as a potential feedstock for the production of various green chemicals and fuels. The high water requirement for the production of microalgae biomass increases the water footprint which is one of the major challenges in the production of microalgae and it might limit the microalgae production. Therefore, recycling of culture medium is necessary to reduce the water footprint of microalgae biomass production. In this study, recycling of culture medium for the cultivation of *Chlorella sorokiniana* (microalgae) and the effect of medium recycling on its growth was investigated. Microalgae were cultivated in recycled spent medium up to three recycled stages. Specific growth rate of microalgae culture in BG-11 medium was found 1.303 Day⁻¹ and it was declined to 1.076 Day⁻¹ after repeated recycling of spent medium. Total dissolved solids increased to 1647 mgL⁻¹ after repeated recycling of spent medium compared to fresh BG-11 medium in which it was estimated to be 824 mgL⁻¹. The concentration of total dissolved solids in spent medium cultures increased to 49.9% as compared to fresh BG-11 medium culture. The decline in growth rate in spent medium was majorly due to inorganic compounds accumulation in the medium.

Keywords: media recycle; microalgae; spent medium

Molecular modeling investigation for novel nutraceuticals against proteases of SARS-CoV-2, H1N1, and Ebola hemorrhagic fever

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Abstract

Global pandemics are serious threats to human life. While well-established and characterized viruses such as The human immunodeficiency virus (HIV) and Hepatitis are still killing millions of people, the emerging viruses are also problematic and have caused several serious outbreaks in recent years, such as the Severe Acute Respiratory Syndrome-Coronavirus (SARS-CoV) in 2002–2003, Swine influenza A (H1N1) in 2009, and Ebola Haemorrhagic fever outbreak in 2014 which has caused thousands of deaths worldwide. The widespread problem of a 2019-novel coronavirus (SARS-CoV-2) strain outbreak has prompted a search for new drugs to protect against these viral infections in the future. It is necessary to immediately investigate this due to the mutation of the viral genome and there being no current protective vaccines or therapeutic drugs. In silico screening, strategies were employed to determine the potential activities of seven HIV protease (HIV-PR) inhibitors, two flu drugs, and four natural nutraceuticals including, gingerols, curcumin, mangiferin, and piperin compounds. The computational approach was carried out to discover the structural modes with a high binding affinity for these nutraceuticals on the homology structure of the coronavirus protease (SARS-CoV-2 PR). From the theoretical calculations, all the nutraceuticals demonstrated various favorable binding affinities. An interesting finding was that nutraceuticals tested had a higher potential binding activity with the pocket sites of SARS-CoV-2 PR compared to the conventional HIV-PR inhibitor drugs. This result supports the idea that all four nutraceuticals could be used individually or in combination to treat viral infections. This study sought to provide fundamental knowledge as preliminary experimental data to propose an existing nutraceutical material against viral infection. Collectively, it is suggested that molecular modeling and molecular docking are suitable tools to search and screen for new drugs and natural compounds that can be used as future treatments for viral diseases.

Keywords: Severe Acute Respiratory Syndrome-Coronavirus (SARS-CoV), Swine influenza A (H1N1), Ebola Haemorrhagic fever, 2019-novel coronavirus (SARS-CoV-2), nutraceuticals, molecular modeling, docking

